-- IN THE SPECIFICATION --

Pages 6 - 7, replace the entire paragraph beginning "Figure 2:" with the following:

- - Figure 2: (A) Schematic representation of a leucine zipper pair visualized from the N-terminus illustrating e/g-interactions and the hydrophobic core formed by the a- and d-positions. (B) Distribution of residues at the semi-randomized positions throughout selection. The number of zipper pairs sequenced is given in parentheses, save "Before selection" where the theoretical distribution is reported. Each pair carries one core a-pair and 6 e/g-pairs. Neutral e/g-pairs have one or both residues as Gln. In "Competition (I114A)" only clones from P6 to P12 (not from earlier passages) were considered for analysis. Thus, 37 individual clones were identified, giving rise to 10 unique sequences due to multiple occurrence of the enriched clones. The distributions were calculated according to the frequency of sequence occurrence (n=37). (C) Leucine zipper sequences WinZip-A1 (SEQ ID NO:1), WinZip-B1 (SEQ ID NO:2), WinZip-A2 (SEQ ID NO:3) and WinZip-B2 (SEQ ID NO:4) obtained after competition selection and chain shuffling. The heptad positions (a to g) are followed by the heptad number (1 to 5). Invariant residues from GCN4 are underlined. Clear boxes indicate the semi-randomized e- and g-positions (black outline) and core a-position (a3) (grey outline). Circled residues were designed to contribute to helix capping. Shaded residues were designed for the introduction of restriction sites. Other residues are from c-Jun (LibA) or c-Fos (LibB). Arrows indicate putative e/g-interactions. --

Page 33, line 6, after "(Gly.Gly.Gly.Gly.Ser)2" please insert --(SEQ ID NO:5)—

Page 70, Please replace the originally filed abstract with the following new abstract:

-- The present invention describes rapid methods to screen for biomolecular interactions in vivo based on protein fragment complementation assays (PCA). We have demonstrated an in vivo library-versus-library screening strategy that has numerous applications in the identification of novel protein-protein interactions and in directed evolution. Also we demonstrate the detection of protein-protein interactions starting with defined (full-length) cDNAs, and the concomitant generation of functional assays that provide initial validation of the cDNA products as being biologically relevant. Also, we screened a large cDNA collection using automated PCA, combined with quantitative detection of protein-protein complexes. The invention enables bait-vs.-library, library-vs.-library and defined gene screening in any type of cell or cellular context, and using a wide range of reporters and detection methods. The invention allows for identifying and validating genes involved in any cellular process and also provide assays to study effects of potential drugs, or gene knockouts on specific pathways.--